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RAW SEQUENCE LISTING              DATE: 12/22/2004
PATENT APPLICATION:  US/10/517,905   TIME: 16:05:53

          Input Set : A:\335026.txt
          Output Set: N:\CRF4\12222004\J517905.raw
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P. 6

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 3 <110> APPLICANT: Oregon Health & Science University
 4         Michael, Heinrich Charles
 5         Corless, Christopher Lee
 6         Fletcher, Jonathan Alfred
 7         Demetri, George D.
 9 <120> TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR
RECEPTOR
10         ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
12 <130> FILE REFERENCE: 899-65892-02
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/517,905
C--> 14 <141> CURRENT FILING DATE: 2004-12-10
14 <150> PRIOR APPLICATION NUMBER: US 60/389,107
15 <151> PRIOR FILING DATE: 2002-06-13
17 <150> PRIOR APPLICATION NUMBER: US 60/438,899
18 <151> PRIOR FILING DATE: 2003-01-08
20 <160> NUMBER OF SEQ ID NOS: 27
22 <170> SOFTWARE: PatentIn version 3.2
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25 <211> LENGTH: 6633
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (395)..(3664)
34 <400> SEQUENCE: 1
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37 gtaagagcaa aaagcgaagg cgcaatctgg acactgggag attcggagcg cagggagttt     120
39 gagagaaact tttattttga agagaccaag gttgagggg ggcttatttc ctgacagcta     180
41 tttacttaga gcaaatgatt agttttagaa ggatggacta taacattgaa tcaattacaa     240
43 aacgcggttt ttgagcccat tactgttgga gctacaggga gagaaacagg aggagactgc     300
45 aagagatcat ttgggaaggc cgtgggcacg ctctttactc catgtgtggg acattcattg     360
47 cggaataaca tcggaggaga agtttcccag agct atg ggg act tcc cat ccg gcg     415
48                                      Met Gly Thr Ser His Pro Ala
49                                       1               5
51 ttc ctg gtc tta ggc tgt ctt ctc aca ggg ctg agc cta atc ctc tgc     463
52 Phe Leu Val Leu Gly Cys Leu Leu Thr Gly Leu Ser Leu Ile Leu Cys
53         10              15              20
55 cag ctt tca tta ccc tct atc ctt cca aat gaa aat gaa aag gtt gtg     511
56 Gln Leu Ser Leu Pro Ser Ile Leu Pro Asn Glu Asn Glu Lys Val Val
57     25              30              35
59 cag ctg aat tca tcc ttt tct ctg aga tgc ttt ggg gag agt gaa gtg     559
60 Gln Leu Asn Ser Ser Phe Ser Leu Arg Cys Phe Gly Glu Ser Glu Val
61 40              45              50              55
63 agc tgg cag tac ccc atg tct gaa gaa gag agc tcc gat gtg gaa atc     607
```

```
64  Ser Trp Gln Tyr Pro Met Ser Glu Glu Glu Ser Ser Asp Val Glu Ile
65              60              65                      70
67  aga aat gaa gaa aac aac agc ggc ctt ttt gtg acg gtc ttg gaa gtg   655
68  Arg Asn Glu Glu Asn Asn Ser Gly Leu Phe Val Thr Val Leu Glu Val
69              75              80                      85
71  agc agt gcc tcg gcg gcc cac aca ggg ttg tac act tgc tat tac aac   703
72  Ser Ser Ala Ser Ala Ala His Thr Gly Leu Tyr Thr Cys Tyr Tyr Asn
73              90              95                      100
75  cac act cag aca gaa gag aat gag ctt gaa ggc agg cac att tac atc   751
76  His Thr Gln Thr Glu Glu Asn Glu Leu Glu Gly Arg His Ile Tyr Ile
77      105             110                     115
79  tat gtg cca gac cca gat gta gcc ttt gta cct cta gga atg acg gat   799
80  Tyr Val Pro Asp Pro Asp Val Ala Phe Val Pro Leu Gly Met Thr Asp
81  120         .           125             130                 135
83  tat tta gtc atc gtg gag gat gat gat tct gcc att ata cct tgt cgc   847
84  Tyr Leu Val Ile Val Glu Asp Asp Asp Ser Ala Ile Ile Pro Cys Arg
85              140             145                 150
87  aca act gat ccc gag act cct gta acc tta cac aac agt gag ggg gtg   895
88  Thr Thr Asp Pro Glu Thr Pro Val Thr Leu His Asn Ser Glu Gly Val
89              155             160                 165
91  gta cct gcc tcc tac gac agc aga cag ggc ttt aat ggg acc ttc act   943
92  Val Pro Ala Ser Tyr Asp Ser Arg Gln Gly Phe Asn Gly Thr Phe Thr
93          170             175                 180
95  gta ggg ccc tat atc tgt gag gcc acc gtc aaa gga aag aag ttc cag   991
96  Val Gly Pro Tyr Ile Cys Glu Ala Thr Val Lys Gly Lys Lys Phe Gln
97      185             190                 195
99  acc atc cca ttt aat gtt tat gct tta aaa gca aca tca gag ctg gat   1039
100 Thr Ile Pro Phe Asn Val Tyr Ala Leu Lys Ala Thr Ser Glu Leu Asp
101 200             205             210                 215
103 cta gaa atg gaa gct ctt aaa acc gtg tat aag tca ggg gaa acg att   1087
104 Leu Glu Met Glu Ala Leu Lys Thr Val Tyr Lys Ser Gly Glu Thr Ile
105             220             225                 230
107 gtg gtc acc tgt gct gtt ttt aac aat gag gtg gtt gac ctt caa tgg   1135
108 Val Val Thr Cys Ala Val Phe Asn Asn Glu Val Val Asp Leu Gln Trp
109             235             240                 245
111 act tac cct gga gaa gtg aaa ggc aaa ggc atc aca atg ctg gaa gaa   1183
112 Thr Tyr Pro Gly Glu Val Lys Gly Lys Gly Ile Thr Met Leu Glu Glu
113         250             255                 260
115 atc aaa gtc cca tcc atc aaa ttg gtg tac act ttg acg gtc ccc gag   1231
116 Ile Lys Val Pro Ser Ile Lys Leu Val Tyr Thr Leu Thr Val Pro Glu
117     265             270                 275
119 gcc acg gtg aaa gac agt gga gat tac gaa tgt gct gcc cgc cag gct   1279
120 Ala Thr Val Lys Asp Ser Gly Asp Tyr Glu Cys Ala Ala Arg Gln Ala
121 280             285             290                 295
123 acc agg gag gtc aaa gaa atg aag aaa gtc act att tct gtc cat gag   1327
124 Thr Arg Glu Val Lys Glu Met Lys Lys Val Thr Ile Ser Val His Glu
125             300             305                 310
127 aaa ggt ttc att gaa atc aaa ccc acc ttc agc cag ttg gaa gct gtc   1375
128 Lys Gly Phe Ile Glu Ile Lys Pro Thr Phe Ser Gln Leu Glu Ala Val
```

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129              315               320               325
131 aac ctg cat gaa gtc aaa cat ttt gtt gta gag gtg cgg gcc tac cca    1423
132 Asn Leu His Glu Val Lys His Phe Val Val Glu Val Arg Ala Tyr Pro
133         330               335               340
135 cct ccc agg ata tcc tgg ctg aaa aac aat ctg act ctg att gaa aat    1471
136 Pro Pro Arg Ile Ser Trp Leu Lys Asn Asn Leu Thr Leu Ile Glu Asn
137     345               350               355
139 ctc act gag atc acc act gat gtg gaa aag att cag gaa ata agg tat    1519
140 Leu Thr Glu Ile Thr Thr Asp Val Glu Lys Ile Gln Glu Ile Arg Tyr
141 360               365               370               375
143 cga agc aaa tta aag ctg atc cgt gct aag gaa gaa gac agt ggc cat    1567
144 Arg Ser Lys Leu Lys Leu Ile Arg Ala Lys Glu Glu Asp Ser Gly His
145             380               385               390
147 tat act att gta gct caa aat gaa gat gct gtg aag agc tat act ttt    1615
148 Tyr Thr Ile Val Ala Gln Asn Glu Asp Ala Val Lys Ser Tyr Thr Phe
149         395               400               405
151 gaa ctg tta act caa gtt cct tca tcc att ctg gac ttg gtc gat gat    1663
152 Glu Leu Leu Thr Gln Val Pro Ser Ser Ile Leu Asp Leu Val Asp Asp
153     410               415               420  ,
155 cac cat ggc tca act ggg gga cag acg gtg agg tgc aca gct gaa ggc    1711
156 His His Gly Ser Thr Gly Gly Gln Thr Val Arg Cys Thr Ala Glu Gly
157     425               430               435
159 acg ccg ctt cct gat att gag tgg atg ata tgc aaa gat att aag aaa    1759
160 Thr Pro Leu Pro Asp Ile Glu Trp Met Ile Cys Lys Asp Ile Lys Lys
161 440               445               450               455
163 tgt aat aat gaa act tcc tgg act att ttg gcc aac aat gtc tca aac    1807
164 Cys Asn Asn Glu Thr Ser Trp Thr Ile Leu Ala Asn Asn Val Ser Asn
165             460               465               470
167 atc atc acg gag atc cac tcc cga gac agg agt acc gtg gag ggc cgt    1855
168 Ile Ile Thr Glu Ile His Ser Arg Asp Arg Ser Thr Val Glu Gly Arg
169             475               480               485
171 gtg act ttc gcc aaa gtg gag gag acc atc gcc gtg cga tgc ctg gct    1903
172 Val Thr Phe Ala Lys Val Glu Glu Thr Ile Ala Val Arg Cys Leu Ala
173     490               495               500
175 aag aat ctc ctt gga gct gag aac cga gag ctg aag ctg gtg gct ccc    1951
176 Lys Asn Leu Leu Gly Ala Glu Asn Arg Glu Leu Lys Leu Val Ala Pro
177     505               510               515
179 acc ctg cgt tct gaa ctc acg gtg gct gct gca gtc ctg gtg ctg ttg    1999
180 Thr Leu Arg Ser Glu Leu Thr Val Ala Ala Ala Val Leu Val Leu Leu
181 520               525               530               535
183 gtg att gtg atc atc tca ctt att gtc ctg gtt gtc att tgg aaa cag    2047
184 Val Ile Val Ile Ile Ser Leu Ile Val Leu Val Val Ile Trp Lys Gln
185             540               545               550
187 aaa ccg agg tat gaa att cgc tgg agg gtc att gaa tca atc agc ccg    2095
188 Lys Pro Arg Tyr Glu Ile Arg Trp Arg Val Ile Glu Ser Ile Ser Pro
189         555               560               565
191 gat gga cat gaa tat att tat gtg gac ccg atg cag ctg cct tat gac    2143
192 Asp Gly His Glu Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp
193         570               575               580
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195 tca aga tgg gag ttt cca aga gat gga cta gtg ctt ggt cgg gtc ttg     2191
196 Ser Arg Trp Glu Phe Pro Arg Asp Gly Leu Val Leu Gly Arg Val Leu
197     585                 590                 595
199 ggg tct gga gcg ttt ggg aag gtg gtt gaa gga aca gcc tat gga tta     2239
200 Gly Ser Gly Ala Phe Gly Lys Val Val Glu Gly Thr Ala Tyr Gly Leu
201 600                 605                 610                 615
203 agc cgg tcc caa cct gtc atg aaa gtt gca gtg aag atg cta aaa ccc     2287
204 Ser Arg Ser Gln Pro Val Met Lys Val Ala Val Lys Met Leu Lys Pro
205                 620                 625                 630
207 acg gcc aga tcc agt gaa aaa caa gct ctc atg tct gaa ctg aag ata     2335
208 Thr Ala Arg Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys Ile
209             635                 640                 645
211 atg act cac ctg ggg cca cat ttg aac att gta aac ttg ctg gga gcc     2383
212 Met Thr His Leu Gly Pro His Leu Asn Ile Val Asn Leu Leu Gly Ala
213             650                 655                 660
215 tgc acc aag tca ggc ccc att tac atc atc aca gag tat tgc ttc tat     2431
216 Cys Thr Lys Ser Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Phe Tyr
217     665                 670                 675
219 gga gat ttg gtc aac tat ttg cat aag aat agg gat agc ttc ctg agc     2479
220 Gly Asp Leu Val Asn Tyr Leu His Lys Asn Arg Asp Ser Phe Leu Ser
221 680                 685                 690                 695
223 cac cac cca gag aag cca aag aaa gag ctg gat atc ttt gga ttg aac     2527
224 His His Pro Glu Lys Pro Lys Lys Glu Leu Asp Ile Phe Gly Leu Asn
225                 700                 705                 710
227 cct gct gat gaa agc aca cgg agc tat gtt att tta tct ttt gaa aac     2575
228 Pro Ala Asp Glu Ser Thr Arg Ser Tyr Val Ile Leu Ser Phe Glu Asn
229             715                 720                 725
231 aat ggt gac tac atg gac atg aag cag gct gat act aca cag tat gtc     2623
232 Asn Gly Asp Tyr Met Asp Met Lys Gln Ala Asp Thr Thr Gln Tyr Val
233             730                 735                 740
235 ccc atg cta gaa agg aaa gag gtt tct aaa tat tcc gac atc cag aga     2671
236 Pro Met Leu Glu Arg Lys Glu Val Ser Lys Tyr Ser Asp Ile Gln Arg
237     745                 750                 755
239 tca ctc tat gat cgt cca gcc tca tat aag aag aaa tct atg tta gac     2719
240 Ser Leu Tyr Asp Arg Pro Ala Ser Tyr Lys Lys Lys Ser Met Leu Asp
241 760                 765                 770                 775
243 tca gaa gtc aaa aac ctc ctt tca gat gat aac tca gaa ggc ctt act     2767
244 Ser Glu Val Lys Asn Leu Leu Ser Asp Asp Asn Ser Glu Gly Leu Thr
245                 780                 785                 790
247 tta ttg gat ttg ttg agc ttc acc tat caa gtt gcc cga gga atg gag     2815
248 Leu Leu Asp Leu Leu Ser Phe Thr Tyr Gln Val Ala Arg Gly Met Glu
249             795                 800                 805
251 ttt ttg gct tca aaa aat tgt gtc cac cgt gat ctg gct gct cgc aac     2863
252 Phe Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn
253             810                 815                 820
255 gtc ctc ctg gca caa gga aaa att gtg aag atc tgt gac ttt ggc ctg     2911
256 Val Leu Leu Ala Gln Gly Lys Ile Val Lys Ile Cys Asp Phe Gly Leu
257     825                 830                 835
259 gcc aga gac atc atg cat gat tcg aac tat gtg tcg aaa ggc agt acc     2959
```

```
260 Ala Arg Asp Ile Met His Asp Ser Asn Tyr Val Ser Lys Gly Ser Thr
261 840                 845             850                 855
263 ttt ctg ccc gtg aag tgg atg gct cct gag agc atc ttt gac aac ctc    3007
264 Phe Leu Pro Val Lys Trp Met Ala Pro Glu Ser Ile Phe Asp Asn Leu
265                 860             865                 870
267 tac acc aca ctg agt gat gtc tgg tct tat ggc att ctg ctc tgg gag    3055
268 Tyr Thr Thr Leu Ser Asp Val Trp Ser Tyr Gly Ile Leu Leu Trp Glu
269             875             880             885
271 atc ttt tcc ctt ggt ggc acc cct tac ccc ggc atg atg gtg gat tct    3103
272 Ile Phe Ser Leu Gly Gly Thr Pro Tyr Pro Gly Met Met Val Asp Ser
273             890             895             900
275 act ttc tac aat aag atc aag agt ggg tac cgg atg gcc aag cct gac    3151
276 Thr Phe Tyr Asn Lys Ile Lys Ser Gly Tyr Arg Met Ala Lys Pro Asp
277         905             910             915
279 cac gct acc agt gaa gtc tac gag atc atg gtg aaa tgc tgg aac agt    3199
280 His Ala Thr Ser Glu Val Tyr Glu Ile Met Val Lys Cys Trp Asn Ser
281 920             925             930             935
283 gag ccg gag aag aga ccc tcc ttt tac cac ctg agt gag att gtg gag    3247
284 Glu Pro Glu Lys Arg Pro Ser Phe Tyr His Leu Ser Glu Ile Val Glu
285             940             945             950
287 aat ctg ctg cct gga caa tat aaa aag agt tat gaa aaa att cac ctg    3295
288 Asn Leu Leu Pro Gly Gln Tyr Lys Lys Ser Tyr Glu Lys Ile His Leu
289             955             960             965
291 gac ttc ctg aag agt gac cat cct gct gtg gca cgc atg cgt gtg gac    3343
292 Asp Phe Leu Lys Ser Asp His Pro Ala Val Ala Arg Met Arg Val Asp
293             970             975             980
295 tca gac aat gca tac att ggt gtc acc tac aaa aac gag gaa gac aag    3391
296 Ser Asp Asn Ala Tyr Ile Gly Val Thr Tyr Lys Asn Glu Glu Asp Lys
297         985                 990             995
299 ctg  aag gac tgg gag ggt  ggt ctg gat gag cag  aga ctg agc gct    3436
300 Leu  Lys Asp Trp Glu Gly  Gly Leu Asp Glu Gln  Arg Leu Ser Ala
301 1000                 1005                 1010
303 gac agt ggc tac atc att  cct ctg cct gac att  gac cct gtc cct    3481
304 Asp  Ser Gly Tyr Ile Ile  Pro Leu Pro Asp Ile  Asp Pro Val Pro
305 1015                 1020                 1025
307 gag  gag gag gac ctg ggc  aag agg aac aga cac  agc tcg cag acc    3526
308 Glu  Glu Glu Asp Leu Gly  Lys Arg Asn Arg His  Ser Ser Gln Thr
309 1030                 1035                 1040
311 tct  gaa gag agt gcc att  gag acg ggt tcc agc  agt tcc acc ttc    3571
312 Ser  Glu Glu Ser Ala Ile  Glu Thr Gly Ser Ser  Ser Ser Thr Phe
313 1045                 1050                 1055
315 atc  aag aga gag gac gag  acc att gaa gac atc  gac atg atg gac    3616
316 Ile  Lys Arg Glu Asp Glu  Thr Ile Glu Asp Ile  Asp Met Met Asp
317 1060                 1065                 1070
319 gac  atc ggc ata gac tct  tca gac ctg gtg gaa  gac agc ttc ctg    3661
320 Asp  Ile Gly Ile Asp Ser  Ser Asp Leu Val Glu  Asp Ser Phe Leu
321 1075                 1080                 1085
323 taa ctggcggatt cgaggggttc cttccacttc tggggccacc tctggatccc         3714
325 gttcagaaaa ccactttatt gcaatgcgga ggttgagagg aggacttggt tgatgtttaa   3774
```

(from Sequence 19)

```
tgtatttgtt cttttttata g ca  aca tca gag ctg gat cta gaa atg gaa    6183
               Ala Thr Ser Glu Leu Asp Leu Glu Met Glu
insert → 210                     215

gct ctt aaa acc gtg tat aag tca ggg gaa acg att gtg gtc acc tgt    6231
Ala Leu Lys Thr Val Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys
220             225             230                     235
```

The above is a sample of several
amino acid numbers inserted in
Sequence 19.

Input Set : **A:\335026.txt**
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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Output Set: **N:\CRF4\12222004\J517905.raw**

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Seq#:19; N Pos. 59841,59842,59843,59844,59845,59846,59847,59848,59849,59850

Input Set : **A:\335026.txt**
Output Set: **N:\CRF4\12222004\J517905.raw**

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:4793 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19
L:4794 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:4901 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19
L:4972 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:10557
M:341 Repeated in SeqNo=19
L:10171 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19
L:10246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:10328 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:10740 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:10886 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:13371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:2047
M:341 Repeated in SeqNo=26
L:13881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:544
M:341 Repeated in SeqNo=27